

GEPHE SUMMARY

ebony (<a +ebony+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=">https://www.gephebase.org/search-criteria?/and+Gene+Gephebase="+ebony+"#gephebase-summary-title)	Gephebase Gene	GP00000252	GepheID
Published	Entry Status	Courtier	Main curator

PHENOTYPIC CHANGE

Morphology (<a +morphology+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait+Category=">https://www.gephebase.org/search-criteria?/and+Trait+Category="+Morphology+"#gephebase-summary-title)	Trait Category		
Coloration (posterior abdomen) (<a +coloration+(posterior+abdomen)+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait=">https://www.gephebase.org/search-criteria?/and+Trait="+Coloration+(posterior+abdomen)+"#gephebase-summary-title)	Trait		
Drosophila melanogaster - Southern Japan; light	Trait State in Taxon A		
Drosophila melanogaster - Southern Japan; dark	Trait State in Taxon B		
Data not curated	Ancestral State		
Intraspecific (<a +intraspecific+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=">https://www.gephebase.org/search-criteria?/and+Taxonomic+Status="+Intraspecific+"#gephebase-summary-title)	Taxonomic Status		
	Taxon A	Taxon B	
Drosophila melanogaster (<a +drosophila+melanogaster+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms="+Drosophila+melanogaster+"#gephebase-summary-title)	Latin Name	Drosophila melanogaster (<a +drosophila+melanogaster+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms="+Drosophila+melanogaster+"#gephebase-summary-title)	Latin Name
fruit fly	Common Name	fruit fly	Common Name
Sophophora melanogaster; fruit fly; Drosophila melanogaster Meigen, 1830; Sophophora melanogaster (Meigen, 1830); Drosophila melangaster	Synonyms	Sophophora melanogaster; fruit fly; Drosophila melanogaster Meigen, 1830; Sophophora melanogaster (Meigen, 1830); Drosophila melangaster	Synonyms
species	Rank	species	Rank
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Holometabola; Diptera; Brachycera; Muscomorpha; Eremoneura; Cyclorrhapha; Schizophora; Acalyptratae; Ephydroidea; Drosophilidae; Drosophilinae; Drosophilini; Drosophila; Sophophora; melanogaster group; melanogaster subgroup	Lineage	cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Holometabola; Diptera; Brachycera; Muscomorpha; Eremoneura; Cyclorrhapha; Schizophora; Acalyptratae; Ephydroidea; Drosophilidae; Drosophilinae; Drosophilini; Drosophila; Sophophora; melanogaster group; melanogaster subgroup	Lineage
melanogaster subgroup () - (Rank: species subgroup) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=32351)	Parent	melanogaster subgroup () - (Rank: species subgroup) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=32351)	Parent
7227 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7227)	NCBI Taxonomy ID	7227 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7227)	NCBI Taxonomy ID
Yes	is Taxon A an Intraspecies?	Yes	is Taxon B an Intraspecies?
Drosophila melanogaster - Southern Japan; light	Taxon A Description	Drosophila melanogaster - Southern Japan; dark	Taxon B Description

GENOTYPIC CHANGE

e	Generic Gene Name	UniProtKB Drosophila melanogaster
ebony; CG3331	Synonyms	O76858 (http://www.uniprot.org/uniprot/O76858)
-	String	AJ224446 (https://www.ncbi.nlm.nih.gov/nucleotide/AJ224446)
-	Sequence Similarities	
GO:0000036 : acyl carrier activity (https://www.ebi.ac.uk/QuickGO/term/GO:0000036)	GO - Molecular Function	
GO:0003833 : beta-alanyl-dopamine synthase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0003833)		
GO:0031177 : phosphantetheine binding		

(<https://www.ebi.ac.uk/QuickGO/term/GO:0031177>)

GO - Biological Process

GO:0048085 : adult chitin-containing cuticle pigmentation

(<https://www.ebi.ac.uk/QuickGO/term/GO:0048085>)

GO:0042417 : dopamine metabolic process

(<https://www.ebi.ac.uk/QuickGO/term/GO:0042417>)

GO:0007623 : circadian rhythm (<https://www.ebi.ac.uk/QuickGO/term/GO:0007623>)

GO:0048082 : regulation of adult chitin-containing cuticle pigmentation

(<https://www.ebi.ac.uk/QuickGO/term/GO:0048082>)

GO:0048066 : developmental pigmentation

(<https://www.ebi.ac.uk/QuickGO/term/GO:0048066>)

GO:0043042 : amino acid adenylation by nonribosomal peptide synthase

(<https://www.ebi.ac.uk/QuickGO/term/GO:0043042>)

GO:0007593 : chitin-based cuticle sclerotization

(<https://www.ebi.ac.uk/QuickGO/term/GO:0007593>)

GO:0048067 : cuticle pigmentation (<https://www.ebi.ac.uk/QuickGO/term/GO:0048067>)

GO:0001692 : histamine metabolic process

(<https://www.ebi.ac.uk/QuickGO/term/GO:0001692>)

GO:0045475 : locomotor rhythm (<https://www.ebi.ac.uk/QuickGO/term/GO:0045475>)

GO:0006583 : melanin biosynthetic process from tyrosine

(<https://www.ebi.ac.uk/QuickGO/term/GO:0006583>)

GO:0048022 : negative regulation of melanin biosynthetic process

(<https://www.ebi.ac.uk/QuickGO/term/GO:0048022>)

GO:0042440 : pigment metabolic process

(<https://www.ebi.ac.uk/QuickGO/term/GO:0042440>)

GO - Cellular Component

GO:0005737 : cytoplasm (<https://www.ebi.ac.uk/QuickGO/term/GO:0005737>)

Presumptive Null

No (<https://www.gephebase.org/search-criteria?/and+Presumptive Null=^No^#gephebase-summary-title>)

Molecular Type

Cis-regulatory (<https://www.gephebase.org/search-criteria?/and+Molecular Type=^Cis-regulatory^#gephebase-summary-title>)

Aberration Type

Unknown (<https://www.gephebase.org/search-criteria?/and+Aberration Type=^Unknown^#gephebase-summary-title>)

Molecular Details of the Mutation

17 nucleotide sites and 2 indels in complete association with the thoracic trident pigmentation intensity in a 13kb region

Experimental Evidence

Linkage Mapping (<https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Linkage Mapping^#gephebase-summary-title>)

Main Reference

Divergent enhancer haplotype of ebony on inversion In(3R)Payne associated with pigmentation variation in a tropical population of *Drosophila melanogaster*. (2011)

(<https://pubmed.ncbi.nlm.nih.gov/21914015>)

Authors

Takahashi A; Takano-Shimizu T

Abstract

The pattern and intensity of pigmentation have direct impact on individual fitness through various ecological factors. In a *Drosophila melanogaster* population from southern Japan, thoracic trident pigmentation intensity of most of the strains could be classified into Dark or Light-type. The expression level variation of the ebony gene correlated well with this phenotype and the allelic differences in expression indicated that the variation is partly due to cis-regulatory changes. In the ~ 4.13 kb gene region, we identified 17 nucleotide sites and 2 indels that were in complete association with the thoracic trident pigmentation intensity. Interestingly, 11 out of 19 sites located within ~ 40.5 kb of the core epidermis enhancer. These sites had no obvious association with the abdominal pigmentation intensity in the previously analysed African populations from Uganda and Kenya, which suggested that multiple potential mutational pathways in the cis-regulatory control region of a single gene could lead to similar phenotypic variation within this species. We also found that the Light-type enhancer haplotype is strongly linked to a cosmopolitan inversion, In(3R)Payne, which is predominant in warmer climatic regions in both hemispheres. The sequence pattern suggested that the strong linkage may be due to selective forces related to thermal adaptation. The inferred selection for lighter pigmentation in the Japanese population is in the opposite direction of the previously reported case of selection for darker individuals in African populations. Nevertheless, both adaptive changes involved cis-regulatory changes of ebony, which shows that this gene is likely to be a common target of natural selection.

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Additional References

RELATED GEPHE

Related Genes

5 (bab, bab1, tan, yellow, wingless (wg)) (<https://www.gephebase.org/search-criteria?/or+Taxon ID=^7227^/and+Trait=Coloration/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

2 (<https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^ebony^/and+Taxon ID=^7227^/or+Gene Gephebase=^ebony^/and+Taxon ID=^7227^#gephebase-summary-title>)

EXTERNAL LINKS

COMMENTS

Contributions of each individual mutation was not tested

